

Figure 1

इं

Ecran Magg113

CTAF

C^{TA}F
 TTTAAAGGGATATGTTTTTCTACTAATG-CtGTAAAAATCACC--AGATTTTTCATTTTcttgaaaaaatgt
 ALLELE 1: 1

ALLELE 2: 1
TTAAAGGGATATGTTTTTCTACTAATGTC-GTAAATAATCACCCCA-ATTTCGCTTTTCTAR

CTAR

CTTACGAAATTC 133

AIIELE 1: 74
tagatataTCATGTTTTTACAAGCATTACAATAATACATCCTGTAATAGG

TCTGTTTCACTCGTATATTAGGAATTC

ECCG_{MAC}405

A2D8F

A2D8F-----ATCAACT'AAAATA-TcTGCA

ATLELE1: 1 TTAAACCTTGGGTGATCGGTATTACAGTACGAGGCCA

TGCA-TAATAATTCCTGGCGCATTGTTTGC

A2D8R

...-aagac-cacatttgagggcatttttgacttgagagactcaggtatcaatcttaa

ALLELE1: 62

AACGATAATTAATTAAGAGAAAGAAC

CTGAGAGAATTCAGGTATCAATCATA

ALLELE2: 74 AACGATAAATATTATTTGGCTTAA

[illegible][illegible]

TTCACCTTGAGCTGA

ADDRESS: 450
MICROSATELLITE
TTCAGAGCCCTGGCGCGGTGGG

ALLELE1: 214 AACGGAAACagagAGAGAGAGAGAGACCTGTCTCAATGCAACCGGCGGCGGAG

TAAGTCTGTTCCAAAGCAACGGGGACAATTAAGCCTGGCGCGCGTG

ALLELE2: 226 AACGGAAC---AGAGAGAGAGGAAGGACCCTTGTCTCTGGGCGGCTTT

CGTCCCTGCTGAAGCAGAGAGGAGAG - CaCGAGA

ALLELE1: 291 GGTCATAAGCGTAACCTGGCCGACGCGGAGT

CGTCCCTTGCTGAAGCAGAGGAGAGGC-CGAGA

ALLELE2: 299 GGTCAA1AAGCGTAACTGGGCTTTT

... 355 CCMAGAGAAACTCCTCGGAAGCAACGGGAATTC 397

[illegible]

NIIEF2: 373 CCAAGAGAACTCTCGGAAGCAACGGGAATTC 405

E_{CGG}M_{AG}116

ALLELE 1: 1 GAATTCGGTTATCTCAACACACTTTTCTGGTTGGTTATAGTAAAGACACAGATTAT
 |||||
 ALLELE 2: 1 GAATTCGGTTATCTCAACACAACTTTTCTGGTTGGTTATAGTAAAGACACAGATTAT
 |||||

ALLELE 1: 60 CCAGGCTTTGAGAGGCATAGAAATAATTTTATATAaAAAAAAGTCTCTTTAA
 |||||
 ALLELE 2: 60 CCAGGCTTTGAGAGGCATAGAAATAATTTTATAT--AAAAAAGTCTCTTTAA
 |||||

E_{ATG}M_{CC}87

allele 1: 1 GAATTCATGGTTCTCTTAT-----GACATTTGCCAAGTAATACTACTATATAAAATTCAGATTTGGGTTT
 |||||
 allele 2: 1 GAATTCATGGTTCTCTTATcttatGACATTTGTTGCCAAGTATACTACTATATAATTCAGATTTGGGTTT
 |||||

allele 1: 68 CTGATAACCGTGGTGGTTAA 87
 |||||

allele 2: 73 CAGATACCGTGGTGGTTAA 92
 |||||

E_{CCC}M_{ATG}161

ALLELE1: 1 TTAATGAAATCGATCAAAATCAAAATAATATATGCTTTTTTAGTTG-gGTCAAGT-ACT
 |||||
 ALLELE2: 1 TTAATGAAATCGATCAAAATCAAAATAATATATGCTTTTTTAGTTGt-gTCAAGTAACT
 |||||

ALLELE1: 61 TTTTATTGAAAAATCGACCCAGTTGAAACACATGTTGAGAAATGTTTGT 116
 |||||
 ALLELE2: 62 TTTTATTGAAAAATCGACCCAGTTGAAACACATGTTGAGAAATGTTTGT 117
 |||||

ALLELE1: 117 GCATCCAAAGTTTTCTGTCAATCAGCTGTGAGAGGGGAATTC 161
 |||||

ALLELE2: 118 GCATCCAAAGTTTTCTGTCAATCAGCTGTGAGAGGGGAATTC 162
 |||||

E_{CC}M_{AG}114

ALLELE1: 1 GAATTCACAGc-AGATTTGATCAAAAGTATTTGTCACAAATGTTCAAGCATCTTA 59
 |||||
 ALLELE2: 1 GAATTCACAG-cAGATTTGATCAAAAGTATTTGTCACAAATGTTCAAGCATCTTA 59
 |||||

ALLELE1: 60 GGGACTGCTATCTTACTCTTAATTTTTTTATTCACATCCAAAGTGTGCTTTAA 114
 |||||
 ALLELE2: 60 GGGAACTGCTATCTTACTCTTAATTTTTTTATTCACATCCAAAGTGTGCTTTAA 114
 |||||

b. $E_{ATG}M_{CGA}87$ BAC extension and TaqMan probe and primers

Allele 1:	ttatcatccaaaattaaaattgaaaactttaatacaaatgcacatttttgaggccattcatgtc
Allele 2:	ttatcatccaaaattaaaattgaaaactttaatacaaatgcacatttttgaggccattcatgtc
	<i>TMA5-F</i>
Allele 1:	atctcttggtcgtgagtccttatcattctctggattgaattcaatggtttctcttat----GACATTGTT
Allele 2:	atctcttggtcgtgagtccttatcattctctggattgaattcaatggtttctcttatGACATTGTT
	<i>TMA5-R</i>
	<i>TMA5-S</i>
Allele 1:	CCCAAGTAATACTACTATATAAATTCAGATTGGTTTCTTGATAACCGTGGTCGTTAAactatatataatacc
Allele 2:	CCCAAGTAATACTACTATATAAATTCAGATTGGTTGGTTTCAGATACCGTGGTCGTTAAactatatataatacc
	<u>ATG4BACF</u>

Figure 2

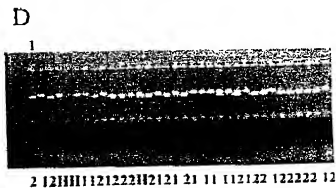
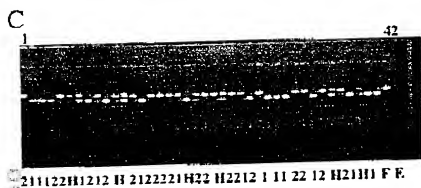
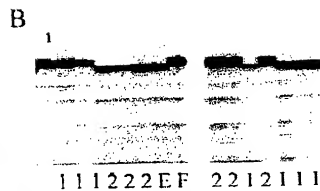
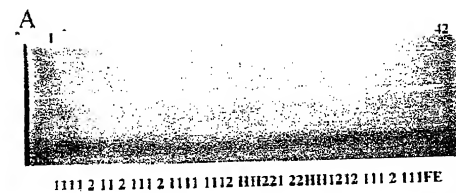
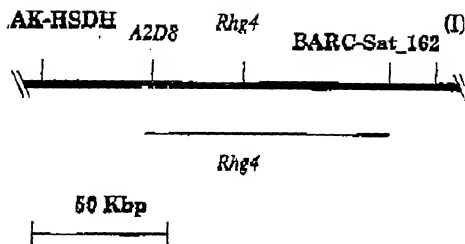


Figure 3



15752434-012004

Figure 4

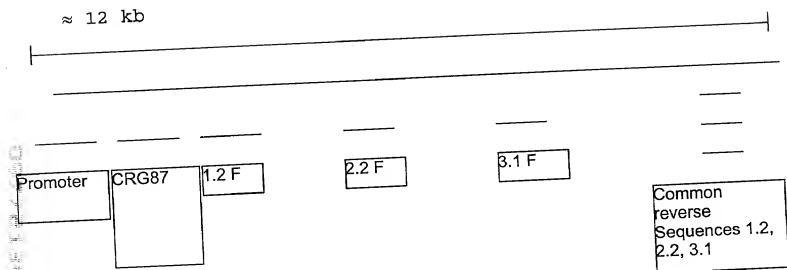
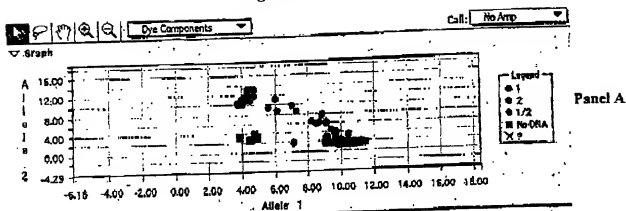


Figure 5



Plate

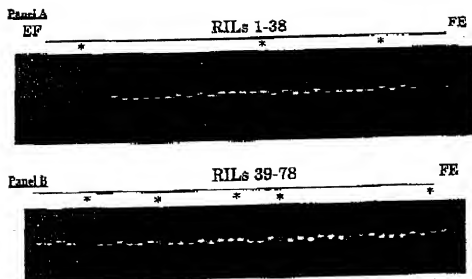
Treat

	1	2	3	4	5	6	7	8	9	10	11	12
A	1	2	1	2	1	1	2	2	1	2	1	2
B	2	1	1	1	1 and 2	1	1	1	1	2	1	2
C	1	1	2	1	1	2	1	2	2	1	1	1
D	1	1	2	2	2	1	2	2	1	1	1	1
E	No Amp	1	2	1	1	No Amp	1	1 and 2	2	1	1	No Amp
F	1	1	1	1	1	1	1	1	2	2	2	No Amp
G	2	1	1 and 2	1	2	1	1	1	1	1	1	No Amp
H	1	1	1	1	1	1	1	2	1	1 and 2	1 and 2	1 and 2

Panel B

2007/03/14 10:00:00

Figure 6



100010-400000

Figure 7A

Synthetic rhg1 gene

1
AATGGGAGGAGTGGGAAAGACAGTGGCTATGGAGCTTGTTCGGGAGGTTGGGTTGGAAT
CAAGTGTGCTCAGGACAGGTTATTGTGATCCAGCTTCCTTGGAGGGTTTGAGGGGTC
GAATCACCGACAAAATTGGCCAACCTCAAGGCCCTCAGGAAGCTTAGTCTTCATGATAAC
CAAAATGGTGTGTTCAATCCCTTCAACTTTGGGACTTCTTCCCAACCTTAGAGGGGTTCA
GTTATTCAACAATAGGCTTACAGGTTCCATACCTCTTTCTTTAGGTTCTGCTTTGGCT
TCAAGTCTCTTGACCTCAGCAACAACCTTGCTCACAGGAGCAATCCCTTATAGTCTTGCT
AATTCACCTAAGCTTTATTGGCTTAACCTTGAGTTTCAACTCCCTCTCTGGTCTTTTACC
AGCTAGCTAACTCACTCATTTTCTCTCACTTTTCTTTCTCTTCAAAATAACAATCTTT
CTGGCTCCCTTCTTAACCTTTGGGGTGGGAATCCAAGAATGGCTCTTTAGGCTTCAA
AATTTGATCCTAGATCATAAATTTTTCACTGGTGACGTTCTGCTCTTTGGGTTAGCTT
AAGAGAGCTCAATGAGATTTCCCTTAGTCTATAATAAGTTTAGTGGAAGCTATACCAAAATG
AAATAGGAACCCCTTTCTAGGCTTAAGACACTTGACATTTCTAATAATGCCTTGAATGGG
AACTTGCTGTACCTCTCTAATTTATCCTCACTTACACTGCTGAATGCAGAGAACA
CCTCCTTGACCTCAATCCCTCAAAGTTTAGGTAGATTGCGTAATCTTTCTGTTTGA
TTTTGAGTAGAAACCAATTTAGTGGACATATTCCTTCAAGCATTGCAACATTTCTCTCG
CTTAGGCAGCTTGATTGTGCTGAATAATTTCAAGTGGAGAAATTCAGGCTCTCTTTGA
CAGTCAGCGCAGCTCTAAATCTCTTCAATGTTTCTCAATAAGCCTCTCAGGTTCTGCTCC
CCCTCTGCTTGCCAAGAAATTTAATCAAGCTCATTTTGTTGGGAAATATTCAACTATGT
GGGTACAGCCCTTCAACCCCATGCTCTTCCCAAGCTCCATCACAAGGAGTCATTGCCCC
ACCTCTGAAGTGTCAAAACATCACCATCATAGGAAGCTAAGCAACAAAGACATAATTC
TCATAGTAGCAGGAGTTCTCCTCGTAGTCTGATTATACCTTTGTTGTGCTGCTTTTC
TGCTTGATCAGAAAAGAGTCAACATCTAGGCCGGGAACGGCAAGCCACCCGAGGGTAG
AGCGGCCACTATGAGGACAGAAAAGGAGTCCCTCCAGTTGCTGGTGGTGATGTTGAAG
CAGGTGGGAGGCTGGAGGGAACTAGTCCATTTTGATGGACCAATGGCTTTTACAGCT
GATGATCTCTTGTGTGCAACAGCTGAGATCATGGGAAAGAGCACCTTAGGAACTGTTTA
TAAGGCTATTTTGGAGGATGGAAGTCAAGTTGCAGTAAAGAGATTGAGGGGAAAGATCA
CTAAAGGTCATAGAGAATTTGAATCAGAAGTCAGTGTTCTAGGAAAATTAGACACCCC
AATGTTTTGGCTCTGAGGGCCTATTACTTGGGACCCAAAGGGGAAAAGCTTCTGGGTTT
TGATACATGCTAAAGGAAGTCTTGCTTCTTCTACATGGAAGGTTCTGTTGCTGGTT
CTTTCATTAAAGTGTGTGTGCTGGTCTTTAATTATAATTTGGAGTTTACCTTAGT
AATCTGTATATAATTTCAATCGGAGAACAGTACAAACAAAAACCTTAAGGAACACACCT
TANCTTTAATATACCATATCAATAAAGTGAATATTTTCTGGTCTATCTTGATCGAGG
GGAAGTGAACATTCTATTATGGCCACAAGATTAAATAGCCCCAAGCCTTGGCCCGGGCT
TGTTTGCTCTTATCCCAGGAGAACATCATACATGGGACCTTNCATCCAGCAATGTGTG
GCTTGATGAAAACAAATGCTAAAAATTCAGATTTTGGCTTTTTCGGGTTGATGTCAAC
TGCTGCTAATTTCAAAGTGTAGCTACAGCTGGAGCATTGGATACCGGGACCTGAGCT
CTCAAAGCTCAAGAAAGCAAACTAAAACTGATATCTACAGTCTTGGTGTATCTTGT
TAGCACTCCTTAACGAGGAATACCTGGGGTGTCTATGAATGGACATAGATTGGCTCAG
TGGGTTGCCCTCAGTTGTCAAAGAGGAGTGGACAAATGAGGTTTTTGATGCAGACTTGAT
GAGAGATGCATCCACAGTTGGCGACGAGTTGCTAAACAGCTTGAAGCTCGCTTTGCACT
GTGTTGATCTTCTCCTCATCAGCACGACCAAGATTCATCAAGTTCTCCAGCAGCTGAAG
AGATTAGACCAGAGAGATCAGTCACAGCCAGTCCCGGGACGATATCGTATAGACAAA
TTTTGCATTGATTTTTTGTGCCAAATGTAGTAGGCCTACTATATATATGTTCTATGAT

067-2334-0320

Figure 7B

TCTTTCATTCTTATATTATTTTTGCCTGTTTGAATGCTGAATTTGTACATACTCATAC
TACAATAAGGTGTAGTTCTGGTTAATTTTACCTCTACCTCAAAGCTGGGGTGTAAATTCT
GTTTCTCCAGGCACATAATAGTTGAAAATAGTTCTCAGGAGCATTCATGTGTTATTC
TGCAAGATTCTCTTTCACGGCTGCTATCTTCTATGCATGCCCTGCCCAT**TAAAT**GCATTA
TGAAGAATTGTAACGGCTGTGTTTTTGGACTTCTTCAAAAAGTTTATGTTATTGCCAGG
TGTATATATCAACATGTTTTAAAGATTTTCAAACAATCAGGTTTTAGATGTGGGTTTGC
ATGCATGAGATTGGACTAGTGCCTTGATGTAGTATAAAATAT**TAAAT**TGTCCAATCAAG
CACCTCTACATGTCCAATAATGGGCCTTATGAACTTAATTTTTTAATTACAACTA
CAGTAATCTTTTGAATAAAGATTTACAAATTACAACNGACATGTGAAGCNGCATCTT
NATTGNCAATCTTCAAGTTACTCTATTATTTTCTGCN

3105bp

CCCTGCTGAATTTGTACATACTCATAC

Figure 7C

Rhg1 Peptide

NGRSGKDSGYGAC**SGGWVG**IKCAQGQVIVIQLPWKGLRGRIT
DKIGQLQGLRKL**SLHDN**QIGGSIPSTLGLLPNLRGVQLFNNRLG
SIP

LSLGFCPLL**QSLDLSNNLLTGAIP**
YSLANSTKLYWLNL**SFNSFSGPLP**
ASLTHSFSLTFL**SLQNNNLSGSLPNSWGG**
NSKNGFFRLQNLILDHNFFTGDVP
ASLGS**LRELNEISLSHN**KFSGAIP
NEIGTL**SRLKTLDISNNAL**GNLP
ATLSNL**SSLTLLNAENNLLDNQIP**
QSLGRLRNLSVLILSRNQFSGHIP
SSIANISSLRQLDLSLNNFSGEIP
VSFDSQRSLNLSNVSYNSLSGSVP

PLLAKKFNSSSFVGN**IQLCGYSP**

STPCL**SQ**

APSQGV**IAPPPEVSKHHHR**

KLSTKDIILIVAGVLLVLIILCCVLLFCLIRKS

TSKAGNGQATEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHF
DGPMAFTADDLLCATAEIMGKSTYGT**VYKAILEDGSQVAVKRLR**
EKITKGHREFESEVSVLGKIRHPNGLALRAYYLGPKGEKLLVFD
YMSKGGLLLFYMEGSCAGSFIKVLCVLVFNYNLEFYLSNLYNSN
RRTVQ**TKTPKEQHLXFNIPYQ**

-SEIFSWSS-CRGN-TFIIGHKMKIXQDLAVACSPSPFETS**YMD**
LXSSNV**CX-NXMLKLQFWSFSVDVNCC-FQRDSYSWSIGIPGT-**
ALKAQESKH-N-YLQSWCYLV**RTPNEEITWGVYEWTRFASVGCL**
SCQRGVDK-GF-CRLDERCIHSWRRVAKHVEARFALC-SFSIS
TTRSSSSSPAAGRD-TREISHSQSHLPGRPLEPYSE**SY**

Figure 7D

Sequences producing significant alignments:		Score (bits)	E Value
pir:T46070	hypothetical protein T18N14.120 - Arabidopsis thaliana	632	e-180
pir:T47727	hypothetical protein F18G21.60 - Arabidopsis thaliana	344	2e-95
pir:T04587	hypothetical protein F23B13.70 - Arabidopsis thaliana	268	9e-71
pir:T49038	hypothetical protein T5P19.20 - Arabidopsis thaliana	257	2e-67
pir:T48210	hypothetical protein T20L15.160 - Arabidopsis thaliana	241	1e-62
pir:T05050	protein kinase homolog M3E9.30 - Arabidopsis thaliana	238	2e-61
pir:T18536	receptor-like protein kinase - Ipomoea nil (Japanese...	236	3e-61
pir:T48489	receptor-like protein kinase - Arabidopsis thaliana	236	5e-61
pir:T10515	disease resistance protein Cf-2.2 - currant tomato	235	6e-61
pir:T10504	disease resistance protein Cf-2.1 - currant tomato	235	6e-61
pir:T30553	disease resistance protein Hcr2-SD - tomato	229	4e-59
pir:S27756	receptor-like protein kinase 5 (EC 2.7.1.-) precursor...	227	1e-58
pir:T48493	receptor-like protein kinase-like protein - Arabidop...	226	3e-58
pir:T46033	receptor protein kinase-like protein - Arabidopsis t...	226	4e-58
pir:T05335	hypothetical protein F1C12.190 - Arabidopsis thaliana	221	1e-56
pir:T0636	hypothetical protein T13K14.100 - Arabidopsis thaliana	219	7e-56
pir:T05898	hypothetical protein F6H11.170 - Arabidopsis thaliana	218	1e-55
pir:T45717	receptor-kinase like protein - Arabidopsis thaliana	212	7e-54
pir:T05322	hypothetical protein F18P4.240 - Arabidopsis thaliana	211	1e-53
pir:T10659	probable serine/threonine-specific protein kinase (E...	211	2e-53
pir:T03784	probable receptor protein kinase - rice	208	1e-52
pir:T50851	receptor protein kinase homolog [imported] - soybean	201	1e-50
pir:T45647	receptor protein kinase-like protein - Arabidopsis t...	199	5e-50
pir:T45718	receptor-kinase like protein - Arabidopsis thaliana	199	7e-50
pir:T50850	receptor protein kinase homolog [imported] - soybean	199	7e-50
pir:T45645	receptor kinase-like protein - Arabidopsis thaliana	196	3e-49
pir:T09356	brassinosteroid-insensitive protein BRI1 - Arabidops...	196	3e-49
pir:T00712	protein kinase homolog F22O13.7 - Arabidopsis thaliana	190	2e-47
pir:A57676	protein kinase Xa21 (EC 2.7.1.-), receptor type prec...	190	3e-47
pir:S39476	kinase-like transmembrane protein TMK1 precursor - ...	188	1e-46
pir:T02154	protein kinase homolog T1P15.2 - Arabidopsis thaliana	188	1e-46
pir:T10725	protein kinase Xa21 (EC 2.7.1.-) AL, receptor type - ...	186	5e-46
pir:T05897	protein kinase homolog F6H11.160 - Arabidopsis thaliana	184	1e-45
pir:T04313	protein kinase Xa21 (EC 2.7.1.-), receptor type - rice	183	3e-45
pir:T10727	protein kinase Xa21 (EC 2.7.1.-) D, receptor type - ...	181	2e-44

Figure 7E

>pir:T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana
Length = 836

Score = 632 bits (1613), Expect = e-180
Identities = 329/550 (59%), Positives = 400/550 (71%), Gaps = 2/550 (0%)
Frame = +1

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Query: 7   RSGKDSGYGACSGGWGIKCAQQQVIVIQLPWKGLGRITDKIGQLQGLRKLKSLHDNQIG 186
          +S +S      GW GIKC +GQV+ IQLPWKGL G I++KIGQL LRKLKSLH+N I
Sbjct: 72  KSWNNSASSQVCSSGWAGIKCLRGQVVAIQLPWKGLGGTISEKIGQLGSLRKLKSLHNNVIA 131

Query: 187 GSIPSTLGLLNPRLRGVQLFNNRLTGSIPLSLGFCLCFKSLDLNNLLTGAIPYSLANSTK 366
          GS+P +LG L +LRGV LFNRL+GSIP+SLG C ++LDLS+N LTGAIP SL ST+
Sbjct: 132 GSVPRSLGVLKSLRGVYLFNNRLSGSIPVSLGNCPLQLQNLDLSSNQLTGAIPPSLTSTR 191

Query: 367 LYWLNLFSNFSFGPLPASLTHSFLSLTFLSLQNNNLSGSLPNSWGGNSKNGFFRLQNLILD 546
          LY LNLFSNFS SGPLP S+ S++LTFL LQ+NNLSGS+P+ + NG L+ L LD
Sbjct: 192 LYRLNLSFNLSLGGPLPVSVARSYTLTFLDLQHNNLSGSIPTDF- - -VNGSHPLKTLNLD 247

Query: 547 HNFPTGDVPASLGLRELNEISLSHNKFSGAIPNEIGTSLRLKTLDISNNALNGNLPATL 726
          HN F+G VP SL L E+S+SHN+ SG+IP E G L L++LD S N++NG +P +
Sbjct: 248 HNRFSGAVPVSLCKHSLLEEVSISHNQLSGSIPRECGLPHLQSLDFSYSINGITIPDSF 307

Query: 727 SNLSSSLTLNLAENNLNDNIQPSLGRRLNLSVLILSRNQFSGHIPSSIANISSRLQLDLS 906
          SNLSSL LN E+N L IP ++ RL NL+ L L RN+ +G IP +I NIS +++LDLS
Sbjct: 308 SNLSSSLVSLNLESNHLKGPIPAIDRLHNLTELNLKRNKINGIPETIGNISGIKKL DLS 367

Query: 907 LNNFSGEIPVFSQDSQSLNLFNVSYNSLGSVPPLLAKKFNSSSVFGNIQLCGYSPSTPC 1086
          NNF+G IP+S L+ FNVSYN+LSG VPP+L+KKFNSSSF+GNIQLCGYS S PC
Sbjct: 368 ENNFTGPIPLSLVHLAKLSSFNVSYNLTSGFPVPPVLSKKFNSSSFLGNIQLCGYSSSNPC 427

Query: 1087 LSQAPSQGVIAAPP--PEVSKHHHHRKSLSTKDIILIVAGVLLVVLIIILCCVLLFLIRKRS 1260
          + + P + + HHHRKLK KD+ILI G LL +L++LCC+LL CLI+KR+
Sbjct: 428 PAPDHHHPLTLSPTSQEPKHHHHRKLSVKDVILIAIGALLAILLLCCILLCCLIKRA 487

Query: 1261 TSRPGTAKPPEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHFDGPMFTAADDLLCATA 1440
          K +G+ T +EK V G AGGE GGLVHFDGP FTADDLLCATA
Sbjct: 488 - - - - -ALQKDGDKDKT--SEKTVSAGVAGTASAGGEMGGKLVHFDGPFVFTADDLLCATA 540

Query: 1441 EIMGKSTYGTGYKAILEDGSAVAVKRLREKITKGHREFESESVLGKIRHPNVLALRAYY 1620
          EIMGKSTYGT YKA LEDG++VAVKRLREK TKG +EFE EV+ LGKIRH N+LALRAYY
Sbjct: 541 EIMGKSTYGTAYKATLEDGNEVAVKRLREKTTKGVKFEFEGETALGKIRHQNLALRAYY 600

Query: 1621 LGPKGEKLLGFD 1656
          LGPKGEKLL FD
Sbjct: 601 LGPKGEKLLVFD 612

```

Figure 7F

Score = 185 bits (464), Expect = 1e-45
Identities = 93/161 (57%), Positives = 122/161 (75%), Gaps = 3/161 (1%)
Frame = +2

Query: 1943 GLVCLHSQENIIHGTSHPMCGLMKNKC*NS--DFGLFRVDVNCC*FQRDSYSWSIGYR 2113
GL LHS EN+IH + ++ ++ N+ D+GL R+ + + ++GYR
Sbjct: 647 GLAHLHSNENMIH--ENLTASNILLDEQTNADYGLSRLMTAAAAATNVIATAGTLGYR 704

Query: 2114 APELSKLLKANTKTDIYSLGVILLELLTRKSPGVSMNGLDLPQWVASVVKKEWTNEVFDA 2293
APE SK+K A+ KTD+YSLG+I+LELLT KSPG NG+DLPOWVAS+VKEWTNEVFD
Sbjct: 705 APEFSKIKNASAKTDVYSLGIILELLTGKSPGEBPTNGMDLPQWVASIVKEWTNEVFDL 764

Query: 2294 DLMRDASTVGDELLNTLKLALHCVDPSPSARPEVHQVLQQLKRL 2425
+LMR+ +VGDELLNTLKLALHCVDPSP+ARPE +QV++QL+ +
Sbjct: 765 ELMRETQSVGDELLNTLKLALHCVDPSPAARPEANQVVEQLEEI 808